

SEQUENCE LISTING

<110> Maliszewski, Charles R.  
Gayle III, Richard B.  
Price, Virginia L.  
Gimpel, Steven D.

<120> Inhibitors of Platelet Activation and Recruitment

<130> 2879-US

<140>

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<150> US 60/104,585

<151> 1998-10-16

<150> US 60/107,466

<151> 1998-11-06

<150> US 60/149,010

<151> 1999-08-13

<150> PCT/US99/22955

<151> 1999-10-13

<160> 31

<170> PatentIn Ver. 2.0

<210> 1

<211> 1599

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (67)..(1596)

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Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser  
1 5 10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156  
Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile  
15 20 25 30

gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204  
Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn  
35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252  
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
50 55 60



tat	aag	aag	gta	gtg	aac	gta	agt	gac	ctt	tac	aag	acc	ccc	tgc	acc	972
Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	
			290			295			300							
aag	aga	ttt	gag	atg	act	ctt	cca	ttc	cag	cag	ttt	gaa	atc	cag	ggt	1020
Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	
			305			310			315							
att	gga	aac	tat	caa	caa	tgc	cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	1068
Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	
			320			325			330							
acc	agt	tac	tgc	cct	tac	tcc	cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	1116
Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	
335			340			345						350				
cca	cca	ctc	cag	ggg	gat	ttt	ggg	gca	ttt	tca	gct	ttt	tac	ttt	gtg	1164
Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	
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atg	aag	ttt	tta	aac	ttg	aca	tca	gag	aaa	gtc	tct	cag	gaa	aag	gtg	1212
Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	
			370			375						380				
act	gag	atg	atg	aaa	aag	ttc	tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	1260
Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	
			385			390			395							
aca	tct	tac	gct	gga	gta	aag	gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	1308
Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	
			400			405			410							
tct	ggg	acc	tac	att	ctc	tcc	ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	1356
Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	
415			420			425						430				
gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc	1404
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	
			435			440			445							
gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc	1452
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	
			450			455			460							
cca	gct	gag	caa	cca	ttg	tcc	aca	cct	ctc	tcc	cac	tcc	acc	tat	gtc	1500
Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr	Tyr	Val	
			465			470			475							
ttc	ctc	atg	ggt	cta	ttc	tcc	ctg	gtc	ctt	ttc	aca	gtg	gcc	atc	ata	1548
Phe	Leu	Met	Val	Leu	Phe	Ser	Leu	Val	Leu	Phe	Thr	Val	Ala	Ile	Ile	
			480			485			490							
ggc	ttg	ctt	atc	ttt	cac	aag	cct	tca	tat	ttc	tgg	aaa	gat	atg	gta	1596
Gly	Leu	Leu	Ile	Phe	His	Lys	Pro	Ser	Tyr	Phe	Trp	Lys	Asp	Met	Val	
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 <213> Homo sapiens

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 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
 35 40 45  
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60  
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 65 70 75 80  
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
 85 90 95  
 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
 100 105 110  
 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
 115 120 125  
 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
 130 135 140  
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
 145 150 155 160  
 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
 165 170 175  
 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
 180 185 190  
 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
 195 200 205  
 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
 210 215 220  
 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
 225 230 235 240  
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
 245 250 255  
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
 260 265 270

10240" 2455350

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu  
465 470 475 480

Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu  
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Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val  
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<210> 3  
<211> 476  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

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TCF40-2475850

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			20					25					30				
Ile	Phe	Leu	Ser	Ser	Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys		
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Tyr	Gly	Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile		
	50					55					60						
Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln		
65					70				75						80		
Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln		
			85						90						95		
Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala		
		100						105					110				
Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu		
		115					120					125					
Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu		
	130					135					140						
Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro		
145					150					155					160		
Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala		
			165						170					175			
Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys		
			180					185					190				
Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr		
		195					200					205					
Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val		
	210					215					220						
Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg		
225					230					235					240		
Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr		
			245					250						255			
Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val		
		260						265					270				
Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys		
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Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg		
	290					295					300						
Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly		
305					310					315					320		

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
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Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
465 470 475

<210> 4  
<211> 476  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<220>  
<221> VARIANT  
<222> (39)  
<223> Any amino acid, preferably Cys or Ser

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Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu  
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
50 55 60

Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	
65					70					75					80	
Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	
			85						90					95		
Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	
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Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	
		115					120					125				
Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	
	130					135					140					
Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	
145					150					155					160	
Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	
			165						170					175		
Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	
			180					185						190		
Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	
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Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	
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Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	
225					230					235					240	
Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	
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Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	
		260					265						270			
Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	
		275					280					285				
Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	
	290					295					300					
Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	
305					310					315					320	
Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	
			325						330					335		
Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	
		340					345						350			
Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys	
		355				360						365				



Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
 370 375 380  
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
 385 390 395 400  
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
 405 410 415  
 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
 420 425 430  
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
 435 440 445  
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
 450 455 460  
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
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<210> 5

<211> 1365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<220>

<221> CDS

<222> (1)..(1362)

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cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg gat	96
Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp	
20 25 30	
gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca gaa	144
Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu	
35 40 45	
aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg gtt	192
Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val	
50 55 60	
aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata ggc	240
Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly	
65 70 75 80	

att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca agg	288
Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg	
85 90 95	
tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg	336
Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met	
100 105 110	
cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat	384
Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp	
115 120 125	
gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc	432
Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala	
130 135 140	
agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc	480
Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile	
145 150 155 160	
aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata	528
Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile	
165 170 175	
gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt	576
Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu	
180 185 190	
ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act atc	624
Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile	
195 200 205	
gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac tac	672
Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr	
210 215 220	
aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca ctc	720
Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu	
225 230 235 240	
tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att ctc	768
Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu	
245 250 255	
agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta agt	816
Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser	
260 265 270	
gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt cca	864
Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro	
275 280 285	
ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc cat	912
Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His	
290 295 300	

caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc cag	960
Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln	
305 310 315 320	
tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt ggg	1008
Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly	
325 330 335	
gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca tca	1056
Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser	
340 345 350	
gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc tgt	1104
Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys	
355 360 365	
gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag gag	1152
Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu	
370 375 380	
aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc ctc	1200
Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu	
385 390 395 400	
ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc cat	1248
Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His	
405 410 415	
ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc tac	1296
Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr	
420 425 430	
atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc aca	1344
Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr	
435 440 445	
cct ctc tcc cac tcc acc taa	1365
Pro Leu Ser His Ser Thr	
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<210> 6

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 6

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Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

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		35					40					45				
Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg	Val	
	50					55					60					
Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	
	65				70					75					80	
Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	
				85					90					95		
Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	
			100					105					110			
Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	
	115						120					125				
Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	
	130					135					140					
Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	
	145				150					155					160	
Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	
				165					170					175		
Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	
			180					185					190			
Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	
		195					200					205				
Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	
	210					215					220					
Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	
	225				230					235					240	
Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	
			245					250						255		
Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	
		260					265						270			
Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	
	275						280					285				
Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	
	290					295				300						
Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	
	305				310					315					320	
Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	
				325				330						335		

Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser  
340 345 350

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys  
355 360 365

Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu  
370 375 380

Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu  
385 390 395 400

Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His  
405 410 415

Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr  
420 425 430

Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr  
435 440 445

Pro Leu Ser His Ser Thr  
450

<210> 7  
<211> 1437  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<220>  
<221> CDS  
<222> (1)..(1434)

<400> 7  
atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96  
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
20 25 30

aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac 144  
Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn  
35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 192  
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
50 55 60

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 240  
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
65 70 75 80

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt	288
His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe	
85 90 95	
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa	336
Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu	
100 105 110	
aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt	384
Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Thr Pro Val	
115 120 125	
tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa	432
Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu	
130 135 140	
gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac	480
Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn	
145 150 155 160	
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa	528
Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu	
165 170 175	
ggg gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt	576
Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser	
180 185 190	
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag	624
Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln	
195 200 205	
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act	672
Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr	
210 215 220	
ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa	720
Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln	
225 230 235 240	
ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg	768
Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu	
245 250 255	
tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att	816
Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile	
260 265 270	
cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga	864
Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly	
275 280 285	
tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc	912
Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr	
290 295 300	

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt	960
Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly	
305 310 315 320	
att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac	1008
Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn	
325 330 335	
acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	1056
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu	
340 345 350	
cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg	1104
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val	
355 360 365	
atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg	1152
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val	
370 375 380	
act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa	1200
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys	
385 390 395 400	
aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt	1248
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe	
405 410 415	
tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca	1296
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr	
420 425 430	
gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc	1344
Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser	
435 440 445	
gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc	1392
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile	
450 455 460	
cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc taa	1437
Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr	
465 470 475	

<210> 8  
 <211> 478  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 8  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
 20 25 30  
 Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn  
 35 40 45  
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
 50 55 60  
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
 65 70 75 80  
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe  
 85 90 95  
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu  
 100 105 110  
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val  
 115 120 125  
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu  
 130 135 140  
 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn  
 145 150 155 160  
 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu  
 165 170 175  
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser  
 180 185 190  
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln  
 195 200 205  
 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr  
 210 215 220  
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln  
 225 230 235 240  
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu  
 245 250 255  
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile  
 260 265 270  
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly  
 275 280 285  
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr  
 290 295 300  
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly  
 305 310 315 320



Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn  
325 330 335

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu  
340 345 350

Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val  
355 360 365

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val  
370 375 380

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys  
385 390 395 400

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe  
405 410 415

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr  
420 425 430

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser  
435 440 445

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile  
450 455 460

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
465 470 475

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser  
20

<210> 10

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
peptide

<400> 10

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 11  
<211> 43  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 11  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys  
35 40

<210> 12  
<211> 29  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 12  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys  
20 25

<210> 13  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 13  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys  
20 25 30

<210> 14  
 <211> 87  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 14  
 ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60  
 tgtccacacc tctctccac gagcccc 87

<210> 15  
 <211> 87  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 15  
 gatcggggct cgtgggagag aggtgtggac aatgggttgc cagctgggat catgttggtc 60  
 aggttcagca ttagcccaa agtccag 87

<210> 16  
 <211> 740  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (42)..(737)

<400> 16  
 cggtagcgcg agcgtcgaca ggcctaggat atcgatacgt a gag ccc aga tct tgt 56  
 Glu Pro Arg Ser Cys  
 1 5  
 gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc 104  
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly  
 10 15 20  
 gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 152  
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 25 30 35  
 atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 200  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 40 45 50

gaa Glu	gac Asp	cct Pro	gag Glu	gtc Val	aag Lys	ttc Phe	aac Asn	tgg Trp	tac Tyr	gtg Val	gac Asp	ggc Gly	gtg Val	gag Glu	gtg Val	248
55					60					65						
cat His	aat Asn	gcc Ala	aag Lys	aca Thr	aag Lys	ccg Pro	cgg Arg	gag Glu	gag Glu	cag Gln	tac Tyr	aac Asn	agc Ser	acg Thr	tac Tyr	296
70					75					80					85	
cgg Arg	gtg Val	gtc Val	agc Ser	gtc Val	ctc Leu	acc Thr	gtc Val	ctg Leu	cac His	cag Gln	gac Asp	tgg Trp	ctg Leu	aat Asn	ggc Gly	344
90					95					100						
aag Lys	gac Asp	tac Tyr	aag Lys	tgc Cys	aag Lys	gtc Val	tcc Ser	aac Asn	aaa Lys	gcc Ala	ctc Leu	cca Pro	gcc Ala	ccc Pro	atg Met	392
105					110					115						
cag Gln	aaa Lys	acc Thr	atc Ile	tcc Ser	aaa Lys	gcc Ala	aaa Lys	ggg Gly	cag Gln	ccc Pro	cga Arg	gaa Glu	cca Pro	cag Gln	gtg Val	440
120					125					130						
tac Tyr	acc Thr	ctg Leu	ccc Pro	cca Pro	tcc Ser	cgg Arg	gat Asp	gag Glu	ctg Leu	acc Thr	aag Lys	aac Asn	cag Gln	gtc Val	agc Ser	488
135					140					145						
ctg Leu	acc Thr	tgc Cys	ctg Leu	gtc Val	aaa Lys	ggc Gly	ttc Phe	tat Tyr	ccc Pro	agg Arg	cac His	atc Ile	gcc Ala	gtg Val	gag Glu	536
150					155					160					165	
tgg Trp	gag Glu	agc Ser	aat Asn	ggg Gly	cag Gln	ccg Pro	gag Glu	aac Asn	aac Asn	tac Tyr	aag Lys	acc Thr	acg Thr	cct Pro	ccc Pro	584
170					175					180						
gtg Val	ctg Leu	gac Asp	tcc Ser	gac Asp	ggc Gly	tcc Ser	ttc Phe	ttc Phe	ctc Leu	tac Tyr	agc Ser	aag Lys	ctc Leu	acc Thr	gtg Val	632
185					190					195						
gac Asp	aag Lys	agc Ser	agg Arg	tgg Trp	cag Gln	cag Gln	ggg Gly	aac Asn	gtc Val	ttc Phe	tca Ser	tgc Cys	tcc Ser	gtg Val	atg Met	680
200					205					210						
cat His	gag Glu	gct Ala	ctg Leu	cac His	aac Asn	cac His	tac Tyr	acg Thr	cag Gln	aag Lys	agc Ser	ctc Leu	tcc Ser	ctg Leu	tct Ser	728
215					220					225						
ccg Pro	ggg Gly	aaa Lys	tga													740
230																

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<210> 17
<211> 232
<212> PRT
<213> Homo sapiens
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Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
1 5 10 15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
85 90 95

Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala  
100 105 110

Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg  
145 150 155 160

His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<210> 18  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 18  
ctttccatcc tgagcaac

18

<210> 19  
<211> 36

<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 19  
aaaaaactag tcagaacaaa gctttgccag aaaacg

36

<210> 20  
<211> 24  
<212> PRT  
<213> Mus sp.

<400> 20  
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile  
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser  
20

<210> 21  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 21  
ctagttctgg agactacaaa gatgacgatg acaaaaccca gaacaa

46

<210> 22  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 22  
agctttgttc tgggttttgt catcgatcatc tttgtagtct ccagaa

46

<210> 23  
<211> 89  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 23  
 ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60  
 tgtccacacc tctctcccac tccacctaa 89

<210> 24  
 <211> 89  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 24  
 ggccttaggt ggagtgggag agaggtgtgg acaatgggtg ctcagctggg atcatgttgg 60  
 tcaggttcag catgtagccc aaagtccag 89

<210> 25  
 <211> 1464  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(1461)

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 25  
 atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15  
 agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96  
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
 20 25 30  
 aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa 144  
 Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys  
 35 40 45  
 acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg 192  
 Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu  
 50 55 60  
 gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca 240  
 Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala  
 65 70 75 80

gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg	288
85 90 95	
gtt aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile	336
100 105 110	
ggc att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro	384
115 120 125	
agg tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly	432
130 135 140	
atg cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu	480
145 150 155 160	
gat gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly	528
165 170 175	
gcc agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr	576
180 185 190	
atc aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser	624
195 200 205	
ata gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp	672
210 215 220	
ctt ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr	720
225 230 235 240	
atc gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp	768
245 250 255	
tac aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala	816
260 265 270	
ctc tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile	864
275 280 285	
ctc agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val	912
290 295 300	



agt gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt	960
Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu	
305 310 315 320	
cca ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc	1008
Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys	
325 330 335	
cat caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc	1056
His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser	
340 345 350	
cag tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt	1104
Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe	
355 360 365	
ggg gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca	1152
Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr	
370 375 380	
tca gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc	1200
Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe	
385 390 395 400	
tgt gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag	1248
Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys	
405 410 415	
gag aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc	1296
Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser	
420 425 430	
ctc ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc	1344
Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile	
435 440 445	
cat ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc	1392
His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly	
450 455 460	
tac atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc	1440
Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser	
465 470 475 480	
aca cct ctc tcc cac tcc acc taa	1464
Thr Pro Leu Ser His Ser Thr	
485	

<210> 26

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 26

Met	Ala	Leu	Trp	Ile	Asp	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	1	5	10	15
Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	20	25	30	
Lys	Thr	Gln	Leu	Thr	Ser	Ser	Gly	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	35	40	45	
Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys	Tyr	Gly	Ile	Val	Leu	50	55	60	
Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile	Tyr	Lys	Trp	Pro	Ala	65	70	75	80
Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg	85	90	95	
Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile	100	105	110	
Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	115	120	125	
Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	130	135	140	
Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu	145	150	155	160
Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	165	170	175	
Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	180	185	190	
Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser	195	200	205	
Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp	210	215	220	
Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr	225	230	235	240
Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp	245	250	255	
Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala	260	265	270	
Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile	275	280	285	
Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val	290	295	300	

Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu  
 305 310 315 320

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys  
 325 330 335

His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser  
 340 345 350

Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe  
 355 360 365

Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr  
 370 375 380

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe  
 385 390 395 400

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys  
 405 410 415

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser  
 420 425 430

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile  
 435 440 445

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly  
 450 455 460

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser  
 465 470 475 480

Thr Pro Leu Ser His Ser Thr  
 485

<210> 27

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 27

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro  
 20 25 30

Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr  
 35 40 45

Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly  
 50 55 60

Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser  
 65 70 75 80  
 Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys  
 85 90 95  
 Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr  
 100 105 110  
 Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu  
 115 120 125  
 Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu  
 130 135 140  
 Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln  
 145 150 155 160  
 Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys  
 165 170 175  
 Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn  
 180 185 190  
 Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln  
 195 200 205  
 Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala  
 210 215 220  
 Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser  
 225 230 235 240  
 Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys  
 245 250 255  
 Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His  
 260 265 270  
 Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro  
 275 280 285  
 Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile  
 290 295 300  
 Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu  
 305 310 315 320  
 Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile  
 325 330 335  
 Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr  
 340 345 350  
 Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu  
 355 360 365

Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu  
 370 375 380  
 Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr  
 385 390 395 400  
 Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His  
 405 410 415  
 Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln  
 420 425 430  
 Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn  
 435 440 445  
 Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 450 455 460

<210> 28

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 28

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu  
20 25 30

Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly  
35 40 45

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys  
50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu  
65 70 75 80

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val  
85 90 95

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu  
100 105 110

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala  
115 120 125

Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp  
130 135 140

Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	
145					150					155					160	
Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	
				165				170						175		
Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	
			180					185					190			
Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	
		195					200					205				
Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	
	210					215					220					
Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	
225					230					235					240	
Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	
				245					250					255		
Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	
			260					265						270		
Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	
		275					280					285				
Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	Phe	Glu	
	290					295					300					
Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	
305					310					315					320	
Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	
				325					330					335		
Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	
			340					345					350			
Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys	Phe	Leu	
		355					360					365				
Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu	Met	Met	
	370					375					380					
Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser	Tyr	Ala	
385					390					395					400	
Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly	Thr	Tyr	
				405					410					415		
Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	Ser	Trp	
			420					425					430			
Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala	Gly	Trp	
		435					440					445				

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln  
 450 455 460

Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470

<210> 29  
 <211> 473  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 29  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15  
 Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr  
 20 25 30  
 Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile  
 35 40 45  
 Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp  
 50 55 60  
 Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu  
 65 70 75 80  
 Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn  
 85 90 95  
 Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val  
 100 105 110  
 Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr  
 115 120 125  
 Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg  
 130 135 140  
 Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe  
 145 150 155 160  
 Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp  
 165 170 175  
 Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp  
 180 185 190  
 Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala  
 195 200 205  
 Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn  
 210 215 220

Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly  
 225 230 235 240  
 Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp  
 245 250 255  
 Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn  
 260 265 270  
 Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val  
 275 280 285  
 Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met  
 290 295 300  
 Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln  
 305 310 315 320  
 Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro  
 325 330 335  
 Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly  
 340 345 350  
 Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn  
 355 360 365  
 Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys  
 370 375 380  
 Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly  
 385 390 395 400  
 Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile  
 405 410 415  
 Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu  
 420 425 430  
 His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr  
 435 440 445  
 Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro  
 450 455 460  
 Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470

<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39



<400> 30

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15

Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu  
20 25 30

Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser  
35 40 45

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val  
50 55 60

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys  
65 70 75 80

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met  
85 90 95

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro  
100 105 110

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser  
115 120 125

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser  
130 135 140

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu  
145 150 155 160

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe  
165 170 175

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn  
180 185 190

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val  
195 200 205

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu  
210 215 220

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe  
225 230 235 240

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp  
245 250 255

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro  
260 265 270

Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys  
275 280 285

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln  
290 295 300

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe  
305 310 315 320

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe  
325 330 335

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe  
340 345 350

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys  
355 360 365

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile  
370 375 380

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys  
385 390 395 400

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe  
405 410 415

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly  
420 425 430

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met  
435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
450 455 460

<210> 31

<211> 58

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys  
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly  
20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu  
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr  
50 55